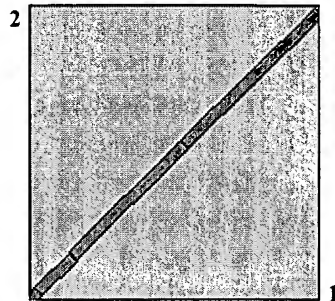


BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.9 [May-01-2004]

Matrix: gap open: gap extension:
 Filter: ☒ Align:
 Propoff: expect: wordsize:

Sequence 1 gi 34855375 cytochrome P450, subfamily 2G, polypeptide 1 [Rattus norvegicus] Length 494 (1 .. 494)

Sequence 2 lcl|seq_2 Length 504 (1 .. 504)



TE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 463 bits (1192), Expect = e-129
 Identities = 228/491 (46%), Positives = 325/491 (65%), Gaps = 3/491 (0%)

```

ry: 1  MALGGAFSIFMTLCLSCLLILIAWKRTSRGGKLPPGPTPIPIFLGNLLQVRIDATFQSFLK 60
    M  G +++ + L L  LL+ +A  T  G LPPGPTP+P LGNLLQ+R  A +  ++
ct: 1  MEATGTWALLLALAL-LLLLTLALSCTRARGHLPPGPTPLPLLGNLLQLRPGALYSGLMR 59

ry: 61 LQKKYGSVFTVYFGP-RPVVILCGHEAVKEALVDQADDFSGRGEMPTLEKNFQGYGLALS 119
    L KKYG VFT+Y GP RPVV+L G EAV+EAL QA++FSGRG +  LE  F G+G+ S
ct: 60 LSKKYGPVFTIYLGWPVRPVVVLVGQEAVEREALGGQAEFSGRGTVAMLEGTDFDGHGVFFS 119

ry: 120 NGERWKILRRFSLTVLRNFGMGKRISIEERIQEEAGYLLEELHKVKGAPIDPTFYLSRTVS 179
    NGERW+ LR+F++ LR+ GMGKR EE IQ EA L+E +G P DP+ L++ S
ct: 120 NGERWRQLRKFTMLALRDLGMGKREGEELIQAEARCLVETFGQTEGRPFDPSSLQAQTS 179

ry: 180 NVICSVVFGKRFDYEDQFRSLMKMINESFVEMSPWAQLYDMYWGVIQYFPGRHNRLYN 239
    NV+CS++FG RF YED+ F++++ + + +S Q Y+M+ ++ PG H +L +
ct: 180 NVVCSLLFGLRFSYEDKEQAVVRAAGTLLGVSSQGGQTYEMFSWFLRPLPGPHKQLLH 239

ry: 240 LIEELKDFIASRVKINEASFDPSPN-RDFIDCFLIKMYQDKSDPHSEXXXXXXXXXXXXXX 298
    + L F +V+ ++ + D S P RD +D FL+KM Q++ +P +E
ct: 240 HVSTLAAFTVRQVQHQGNLDASGPARDLVDAFLKMAQEEQNPGTEFTNKNMLMTVIYL 299

ry: 299 XXAGTETVSSTLRYGFLLLMKYPEVEAKIHEEINQVIGTHRTPRVDDRAKMPYTDABIHE 358
    AGT TVS+T+ Y LLLMKYP V+ + EE+N+ +G + P + DR ++PYTDAV+HE
ct: 300 LFAGTMTVSTTVGYTLTLLMKYPHVQKWVREELNRELGAGQAPSLGDRTRLPYTDAVLHE 359

ry: 359 IQRLTDIVPLGVPHNVIRDTHFRGYFLPKGTDVYPLIGSVLKDPKYFRYPEAFYPQHFLD 418
    QRL +VP+G+P ++R T FRGY LP+GT+V+PL+GS+L DP F++PE F P FLD
ct: 360 AQRLLALVPMGIPRTLMTTRFRGYTLQGTVEVFPPLGSLHDPNIFKHPEEFNPDRFLD 419

ry: 419 EQGRFKNDFAVAFSSGKRICVGEALARMELFLYFTSILQRFSLRSLVPPADIDIAHKIS 478
    GRF+K++AF+ FS GKR+C+GE LA+ ELFL+FT+ILQ FSL S PP + + +S
ct: 420 ADGRFRKHEAFLPFSLGKRVCLEGLAKAELFLFTTILQAFSLESPPCDTLSTLKPTVS 479

ry: 479 GFGNIPPTYEL 489
    G NIPP ++L
ct: 480 GLFNIPPAFQL 490
  
```

Time: 0.03 user secs. 0.00 sys. secs 0.03 total secs.

dbda K H
 0.325 0.142 0.434

ped
 dbda K H
 0.267 0.0410 0.140

ix: BLOSUM62
Penalties: Existence: 11, Extension: 1
er of Sequences: 1
er of Hits to DB: 1725
er of extensions: 1047
er of successful extensions: 4
er of sequences better than 10.0: 1
er of HSP's better than 10.0 without gapping: 1
er of HSP's gapped: 1
er of HSP's successfully gapped: 1
er of extra gapped extensions for HSPs above 10.0: 0
th of query: 494
th of database: 679,922,428
th adjustment: 133
ctive length of query: 361
ctive length of database: 679,922,295
ctive search space: 245451948495
ctive search space used: 245451948495
hboring words threshold: 9
low for multiple hits: 0
15 (7.0 bits)
129 (50.0 bits)
129 (50.0 bits)
40 (22.0 bits)
78 (34.7 bits)